

REMARKS

Claim Status/Support For Claim Amendment

Claim 1 has been amended. Claims 2-35 have been cancelled. Claims 36-43 have been added. Claims 1 and 36-43 are pending in the instant application.

The above additions to the claims find basis in the original disclosure at page 12, lines 2-12 and page 17 lines 7-14. The method of new claim 36 is described in detail at pages 20-27. Page 28 line 11 to page 29, line 7 refers to the use of various types of samples. Page 20, lines 2-6 refer specifically to the use of SELDI MS techniques in the methods of the instant invention. Page 18, lines 5-7 describe kits contemplated for use with the biopolymer marker of the instant invention. It is clear from these specific recitations and from the description of methods utilized that the methods and types of kits recited in the newly added claims (36-43) were fully contemplated by the inventors at the time of filing and were enabled by virtue of the disclosure as originally filed.

Sequence Compliance

Applicants have reviewed the entire specification including the figures and the claims for sequence disclosures. The only sequence found to be disclosed is the amino acid sequence identified as SEQ ID NO:1. Applicants provided a Sequence

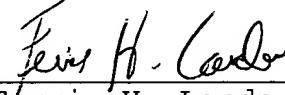
Listing (in both paper and computer readable form) disclosing SEQ ID NO:1 on April 19, 2002. However, Applicants noted that the first and last amino acid residues of SEQ ID NO:1 were not included in the originally filed Sequence Listing. Applicants herein provide a diskette containing a substitute Sequence Listing in electronic computer readable form to replace the previously submitted copy (filed on April 19, 2002). The diskette submitted herewith contains a Sequence Listing which adds the first and last amino acid residues to SEQ ID NO:1. As shown in Figure 1, the marker identified in patient sera consists of amino acid residues 2-12 of SEQ ID NO:1, the first and last amino acid residues shown in parentheses are predicted. When carrying out mass spectrometric procedures, it is possible to fragment a whole molecule, depending upon the enzyme used for digestion. A sequence is often predicted from these fragments but often the sequence is not identified completely. It is conventional in the art to show the missing portions of the predicted sequence in parentheses. The first and last amino acid residues of SEQ ID NO:1 are predicted residues as indicated by the parentheses in Figure 1. The peptide sequence without the predicted first and last amino acid residues was shown in the original specification at page 27, line 18 and is shown in the figures with the first and last predicted amino acid residues. Thus, no new matter is added, the substitute Sequence Listing is

for the purpose of clarifying the use of parentheses only. Applicants also herein provide a substitute paper copy of the Sequence Listing as contained on the diskette filed herewith. The computer readable form of the substitute Sequence Listing is identical to the paper copy of the substitute Sequence Listing. The amendments to the claims and specification limiting the marker sequences to specific amino acid residues are also made for the purpose of clarification only. The claims as herein amended limit the marker sequence to amino acid residues 2-12 of SEQ ID NO:1.

Conclusion

Now that applicants have fully responded to the Office Action mailed on March 27, 2003, an examination on the merits is respectfully requested.

Respectfully submitted,

  
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